

9904247_1.Dna /rev

Emfun:Scl9354

ID SCL9354 standard; DNA; FUN; 15693 BP.
 AC U53878; Y13138;
 SV U53878.1
 DT 10-APR-1996 (Rel. 47, Created)
 DT 23-AUG-1997 (Rel. 52, Last updated, Version 3)
 DE Saccharomyces cerevisiae chromosome XII cosmid 9354.
 KW .
 OS Saccharomyces cerevisiae (baker's yeast)
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP 1-15693
 RX MEDLINE; 97313267.
 RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
 RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A., Entian K.D.,
 RA Floeth M., Goffeau A., Hebling U., Heumann K., Heuss-Neitzel D.,
 RA Hilbert H., Hilger F., Kleine K., Kotter P., Louis E.J., Messenguy F.,
 RA Mewes H.W., Miosga T., Mostl D., Muller-Auer S., Nentwich U., Obermaier B.,
 RA Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S.,
 RA Rieger M., Rinke M., Rose M., Scharfe M., Scherens B., Scholler P.,
 RA Schwager C., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M.,
 RA Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R.,
 RA Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII";
 RL Nature 387(6632):0-0(0).
 RN [2]
 RP 1-15693
 RA Geisel C.;
 RT "The sequence of S. cerevisiae cosmid 9354";
 RL Unpublished.
 RN [3]
 RP 1-15693
 RA Waterston R.;
 RT ;
 RL Submitted (08-APR-1996) to the EMBL/GenBank/DDBJ databases.
 RL Robert Waterston
 RN [4]
 RP 1-15693
 RA Cherry J.M.;
 RT ;
 RL Submitted (22-AUG-1997) to the EMBL/GenBank/DDBJ databases.
 RL Saccharomyces Genome Database
 DR SPTREMBL; Q12090; Q12090.
 DR SPTREMBL; Q12102; Q12102.
 DR SPTREMBL; Q12130; Q12130.
 DR SPTREMBL; Q12259; Q12259.
 DR SPTREMBL; Q12500; Q12500.
 DR SPTREMBL; Q12528; Q12528.
 DR SWISS-PROT; P32485; HOG1_YEAST.
 DR SWISS-PROT; P38013; PM20_YEAST. . . .

SCORES Init1: 2446 Initn: 2446 Opt: 2446 z-score: 1683.2 E(): 0
 99.8% identity in 491 bp overlap

9904247_1.Dn			489	479	469	
			ATGTGATATAGTGT	TAAAGCGAATGACAGAAGA		
Scl9354	GATAGAAGCGACAGTAGAAAATTGCATTATTGATATAGTGT	TAAAGCGAATGACAGAAGA				
	5140	5150	5160	5170	5180	5190
	459	449	439	429	419	409

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9904247_1.Dn TTAATTTCTTGGTATGTTAGGAAAGAATAAAGGAGAATAAGAATAATTAGAACAAATGTAG
Sc19354      TTAATTTCTTGGTATGTTAGGAAAGAATAAAGGAGAATAAGAATAATTAGAACAAATGTAG
              5200      5210      5220      5230      5240      5250
9904247_1.Dn 399      389      379      369      359      349
Sc19354      GATGGAAAGAAAGATTATCAAGCATGCCGACTTTATATACTTGAACGGAGGCAAAGGATG
              GATGGAAAGAAAGATTATCAAGCATGCCGACTTTATATACTTGAACGGAGGCAAAGGATG
              5260      5270      5280      5290      5300      5310
9904247_1.Dn 339      329      319      309      299      289
Sc19354      CAAAATTTTCTCACATTTCTTTCTGCCGTTATGTTGGGAGTAAGACTCCCATTATCGCAA
              CAAAATTTTCTCACATTTCTTTCTGCCGTTATGTTGGAAGTAAGACTCCCATTATCGCAA
              5320      5330      5340      5350      5360      5370
9904247_1.Dn 279      269      259      249      239      229
Sc19354      TACTGCAACACGAATATGCAAATTTGCTGAGTTATCGCAGATAGTTGTTGCAAAGATAG
              TACTGCAACACGAATATGCAAATTTGCTGAGTTATCGCAGATAGTTGTTGCAAAGATAG
              5380      5390      5400      5410      5420      5430
9904247_1.Dn 219      209      199      189      179      169
Sc19354      CGGCGTAGGTGGCCGCGAAATGGGGAATTCCAAAACAAACGGTTTTTTTACTCCTGAGAA
              CGGCGTAGGTGGCCGCGAAATGGGGAATTCCAAAACAAACGGTTTTTTTACTCCTGAGAA
              5440      5450      5460      5470      5480      5490
9904247_1.Dn 159      149      139      129      119      109
Sc19354      ATACTTGACGGGATAATCCAGGGCCTACCAACCCACGCTTCGAGGATTGGCTTTTATTTT
              ATACTTGACGGGATAATCCAGGGCCTACCAACCCACGCTTCGAGGATTGGCTTTTATTTT
              5500      5510      5520      5530      5540      5550
9904247_1.Dn 99      89      79      69      59      49
Sc19354      TTTTTTTTTTGGTGGCGTTTTATTTCTTTCCCGCTTTCTGGGACTTGTGCGGAGTTTGTAG
              TTTTTTTTTTGGTGGCGTTTTATTTCTTTCCCGCTTTCTGGGACTTGTGCGGAGTTTGTAG
              5560      5570      5580      5590      5600      5610
9904247_1.Dn 39      29      19      9
Sc19354      AGGGGCGCGCGGCAAAGGATTCCCAAACGGAAATCAGACG
              AGGGGCGCGCGGCAAAGGATTCCCAAACGGAAATCAGACGCCAATAGCCAGCACTCAAA
              5620      5630      5640      5650      5660      5670
Sc19354      GCAGTTCTGGACCCATTCCGATTTTCCCATTTGTTTCTTGC GCGTGCTGATTCCGACACG
              5680      5690      5700      5710      5720      5730
9904247_1.Dna /rev
Emfun:Scchxiila

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ID SCCHXIILA standard; DNA; FUN; 37639 BP.
 AC X89514;
 SV X89514.1
 DT 03-MAY-1996 (Rel. 47, Created)
 DT 14-APR-1997 (Rel. 51, Last updated, Version 4)
 DE S.cerevisiae DNA from chromosome XII right arm
 KW aspartyl protease; HOG1 gene; mitogen-activated protein kinase;
 KW small nuclear RNA U6 protein; SNR6 gene; YAP3 gene.
 OS Saccharomyces cerevisiae (baker's yeast)
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

OC Saccharomycetaceae; Saccharomyces.

RN [1]
 RA Verhasselt P., Volckaert G.;
 RT "Sequence analysis of a 37.6 kbp cosmid clone from the right arm of
 RT Saccharomyces cerevisiae chromosome XII, carrying YAP3, HOG1, SNR6,
 RT tRNA-Arg3 and 23 new open reading frames, among which several homologies
 RT to proteins involved in cell division control and to mammalian growth
 RT factors and other animal proteins are found";
 RL Yeast 13:241-250(1997).
 RN [2]
 RA Volckaert G.;
 RT ;
 RL Submitted (07-JUL-1995) to the EMBL/GenBank/DDBJ databases.
 RL G. Volckaert, Laboratory of Gene Technology, Catholic University of Leuven,
 RL Willem de Croylaan, B-3001 Leuven, BELGIUM
 RN [3]
 RP 1-37639
 RA Volckaert G.;
 RT ;
 RL Submitted (20-SEP-1995) to the EMBL/GenBank/DDBJ databases.
 RL G. Volckaert, Laboratory of Gene Technology, Catholic University of Leuven,
 RL Willem de Croylaan 42, B-3001 Leuven, BELGIUM
 DR SPTREMBL; Q05382; Q05382.
 DR SPTREMBL; Q05383; Q05383.
 DR SPTREMBL; Q05385; Q05385.
 DR SPTREMBL; Q12090; Q12090.
 DR SPTREMBL; Q12102; Q12102.
 DR SPTREMBL; Q12130; Q12130.
 DR SPTREMBL; Q12138; Q12138.
 DR SPTREMBL; Q12174; Q12174.
 DR SPTREMBL; Q12186; Q12186.
 DR SPTREMBL; Q12259; Q12259.
 DR SPTREMBL; Q12288; Q12288.
 DR SPTREMBL; Q12309; Q12309.
 DR SPTREMBL; Q12312; Q12312.
 DR SPTREMBL; Q12354; Q12354.
 DR SPTREMBL; Q12395; Q12395.
 DR SPTREMBL; Q12440; Q12440.
 DR SPTREMBL; Q12500; Q12500.
 DR SPTREMBL; Q12528; Q12528. . . .

SCORES Initl: 2446 Initn: 2446 Opt: 2446 z-score: 1679.7 E(): 0
 99.8% identity in 491 bp overlap

		489	479	469	
9904247_1.Dn		ATGTGATATAGTGTTTAAGCGAATGACAGAAGA			
Scchxiila		GATAGAAGCGACAGTAGAAAATTGCATTATTGATATAGTGTTTAAGCGAATGACAGAAGA			
	6680	6690	6700	6710	6720 6730
	459	449	439	429	419 409
9904247_1.Dn	TTAATTTCTTGGTATGTTAGGAAAGAATAAAGGAGAATAAGAATAATTAGAACAATGTAG				
Scchxiila	TTAATTTCTTGGTATGTTAGGAAAGAATAAAGGAGAATAAGAATAATTAGAACAATGTAG				
	6740	6750	6760	6770	6780 6790
	399	389	379	369	359 349
9904247_1.Dn	GATGGAAAGAAAGATTATCAAGCATGCCGACTTTATATACTTGAACGGAGGCAAAGGATG				
Scchxiila	GATGGAAAGAAAGATTATCAAGCATGCCGACTTTATATACTTGAACGGAGGCAAAGGATG				
	6800	6810	6820	6830	6840 6850
	339	329	319	309	299 289

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9904247_1.Dn CAAAATTTTCTCACATTTCTTTCTGCCGTTATGTTGGGAGTAAGACTCCCATTATCGCAA
|||
Scchxiila CAAAATTTTCTCACATTTCTTTCTGCCGTTATGTTGGAAGTAAGACTCCCATTATCGCAA
6860 6870 6880 6890 6900 6910

279 269 259 249 239 229
9904247_1.Dn TACTGCAACACGAATATGCAAATTTGCTGAGTTATCGCAGATAGTTGTTGCAAAGATAG
|||
Scchxiila TACTGCAACACGAATATGCAAATTTGCTGAGTTATCGCAGATAGTTGTTGCAAAGATAG
6920 6930 6940 6950 6960 6970

219 209 199 189 179 169
9904247_1.Dn CGGCGTAGGTGGCCGCGAAATGGGGAATTCCAAAACAAACGGTTTTTTTACTCCTGAGAA
|||
Scchxiila CGGCGTAGGTGGCCGCGAAATGGGGAATTCCAAAACAAACGGTTTTTTTACTCCTGAGAA
6980 6990 7000 7010 7020 7030

159 149 139 129 119 109
9904247_1.Dn ATACTTGACGGGATAATCCAGGGCCTACCACCCACGCTTCGAGGATTGGCTTTTATTTT
|||
Scchxiila ATACTTGACGGGATAATCCAGGGCCTACCACCCACGCTTCGAGGATTGGCTTTTATTTT
7040 7050 7060 7070 7080 7090

99 89 79 69 59 49
9904247_1.Dn TTTTTTTTTGGTGGCGTTTTATTTCTTTCCCGCTTTCTGGGACTTGTGCGGAGTTTTGAG
|||
Scchxiila TTTTTTTTTGGTGGCGTTTTATTTCTTTCCCGCTTTCTGGGACTTGTGCGGAGTTTTGAG
7100 7110 7120 7130 7140 7150

39 29 19 9
9904247_1.Dn AGGGGCGCGCGGCAAAGGATTCCCAAACGGAATCAGACG
|||
Scchxiila AGGGGCGCGCGGCAAAGGATTCCCAAACGGAATCAGACGCCAATAGCCAGCACTCAAA
7160 7170 7180 7190 7200 7210

Scchxiila GCAGTTCTGGACCCATTCCGATTTTCCCATTTGGTTCTTGCGCGTGCTGATTCCGACACG
7220 7230 7240 7250 7260 7270

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9904247_1.Dna
Emgss6:Aq492301

ID AQ492301 standard; DNA; GSS; 630 BP.
AC AQ492301;
SV AQ492301.1

DT 27-APR-1999 (Rel. 59, Created)
DT 04-MAR-2000 (Rel. 63, Last updated, Version 2)
DE V119H10 mTn-3xHA/lacZ Insertion Library *Saccharomyces cerevisiae* genomic
DE 5', genomic survey sequence.
KW GSS.
OS *Saccharomyces cerevisiae* (baker's yeast)
OC Eukaryota; Fungi; Ascomycota; *Saccharomycetes*; *Saccharomycetales*;
OC *Saccharomycetaceae*; *Saccharomyces*.
RN [1]
RP 1-630
RA Ross-Macdonald P., Roemer T., Coelho P.S.R., Agarwal S., Kumar A.,
RA desEtages S.A., Cheung K.-H., Sheehan A., Symoniatis D., Jansen R.,
RA Umansky L., Heidtman M., Nelson K., Iwasaki H., Kanada D., Lugo R.,
RA Hager K., Miller P., Roeder G.S., Snyder M.;
RT "Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene
RT Disruption";
RL Unpublished.
CC Contact: Kumar A
CC Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
CC Yale University